



TECHNISCHE
UNIVERSITÄT
DRESDEN

Center for Information Services and High Performance Computing (ZIH)

ORNL Vampir/VampirTrace Training

Performance Analysis for Hardware Accelerators

Jens Doleschal (jens.doleschal@tu-dresden.de)

Guido Juckeland (guido.juckeland@tu-dresden.de)



Agenda

Motivation / Vendor Support

VampirTrace API Tracing

VampirTrace CUDA Support

An example: PiConGPU

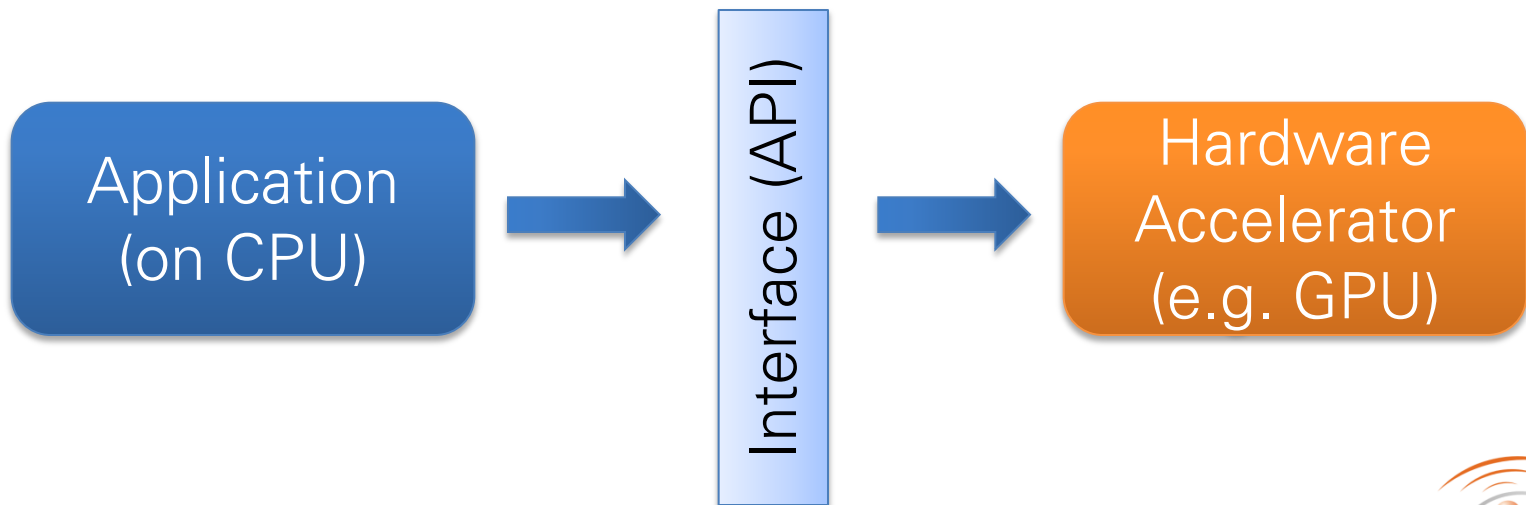
Summary / Outlook

Motivation / Vendor Support

Motivation

- Single CPU performance stagnating since 2004
- Solution of the CPU vendors → multiple CPU cores on one chip
- BUT: This requires parallelization of the applications to make use of all cores
- (Re-) Appearance of Hardware Accelerators to offer even more performance

Running an accelerated application:



Potential Performance Problems

Accelerator code is
(automatically) generated

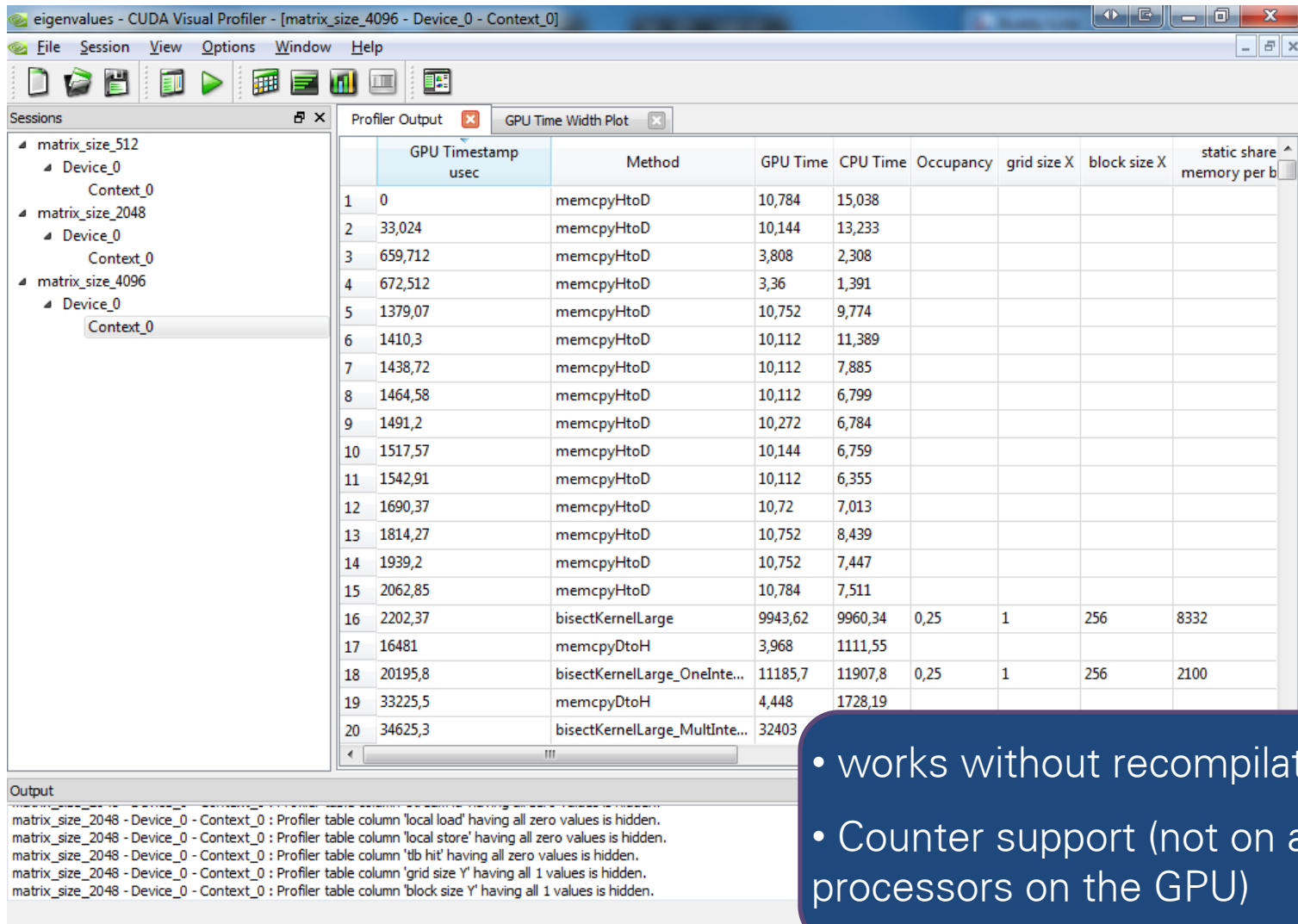
Accelerator is running its own
program code

Not enough
insight into the
program execution

Performance monitoring
hardware on the accelerator
not/poorly exposed to user over
the API

Using accelerators adds another
level of complexity to (parallel)
programming

CUDA Visual Profiler (Eigenvalues; Profiler Output)



The screenshot displays the CUDA Visual Profiler window for the 'eigenvalues' application. The left sidebar shows the session hierarchy: matrix_size_512, matrix_size_2048, and matrix_size_4096, each with Device_0 and Context_0. The main area shows the 'Profiler Output' table with the following columns: GPU Timestamp (usec), Method, GPU Time, CPU Time, Occupancy, grid size X, block size X, and static share memory per b. The table contains 20 rows of data, showing various methods like memcpyHtoD and bisectKernelLarge. A blue callout box on the right contains the following text:

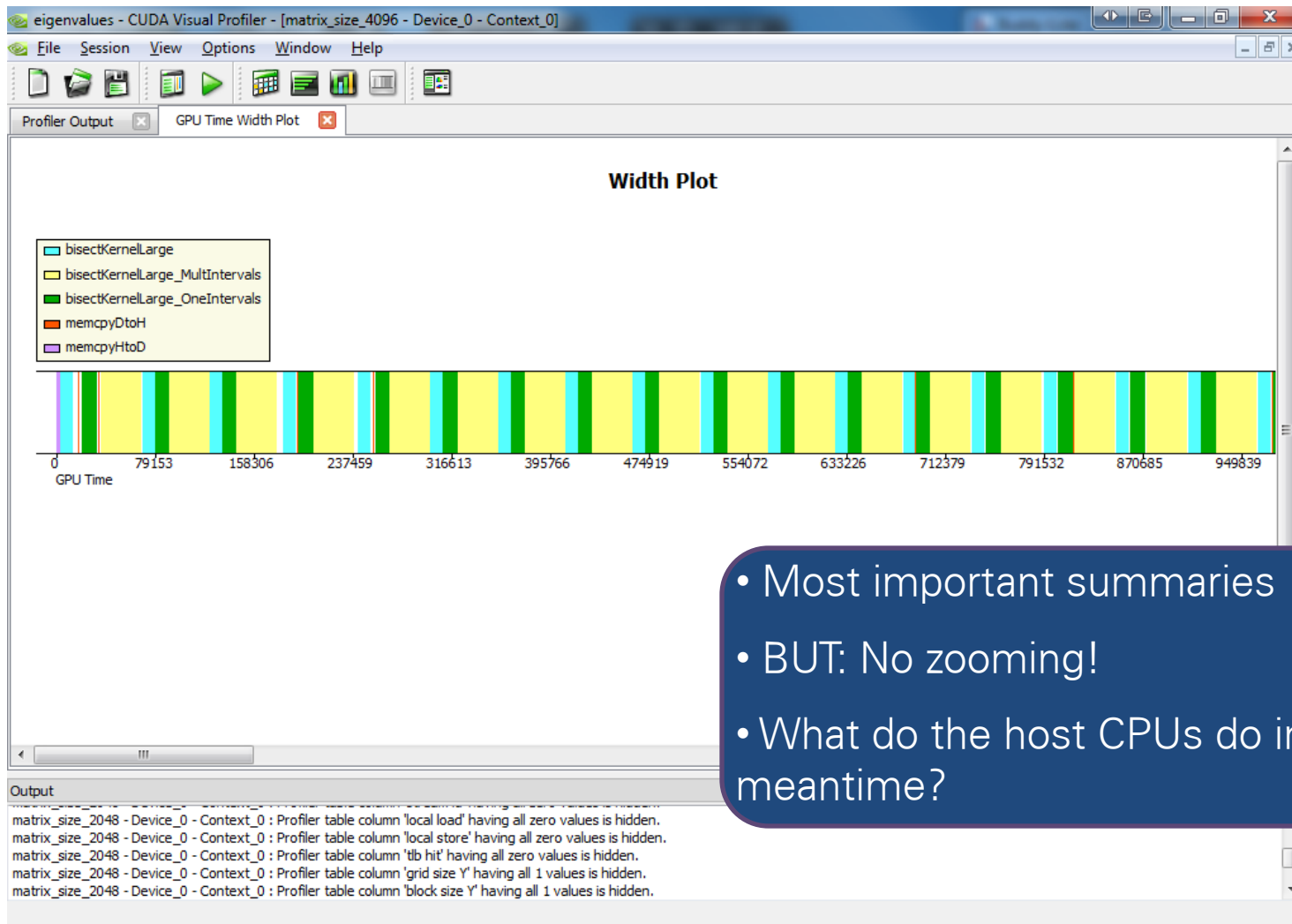
- works without recompilation
- Counter support (not on all processors on the GPU)

- Profiling possible in every Cuda-Application without recompilation
 - Control via environment variables and config file
 - Output file with counters will be generated
 - Different counter values collectable BUT only 4 on one run
 - Multiple runs to collect all counters
- Counters
 - For single multiprocessor
 - Cumulative count for all thread blocks on multiprocessor 0
 - Examples: **branch**, **instructions**
 - For a Texture Processing Cluster (TPC); Examples:
 - **Gld uncoalesced**: Number of non-coalesced global memory loads
 - **Local load**: Number of local memory loads
 - **Tlb miss**: Number of instruction or constant memory cache misses

CUDA Visual Profiler

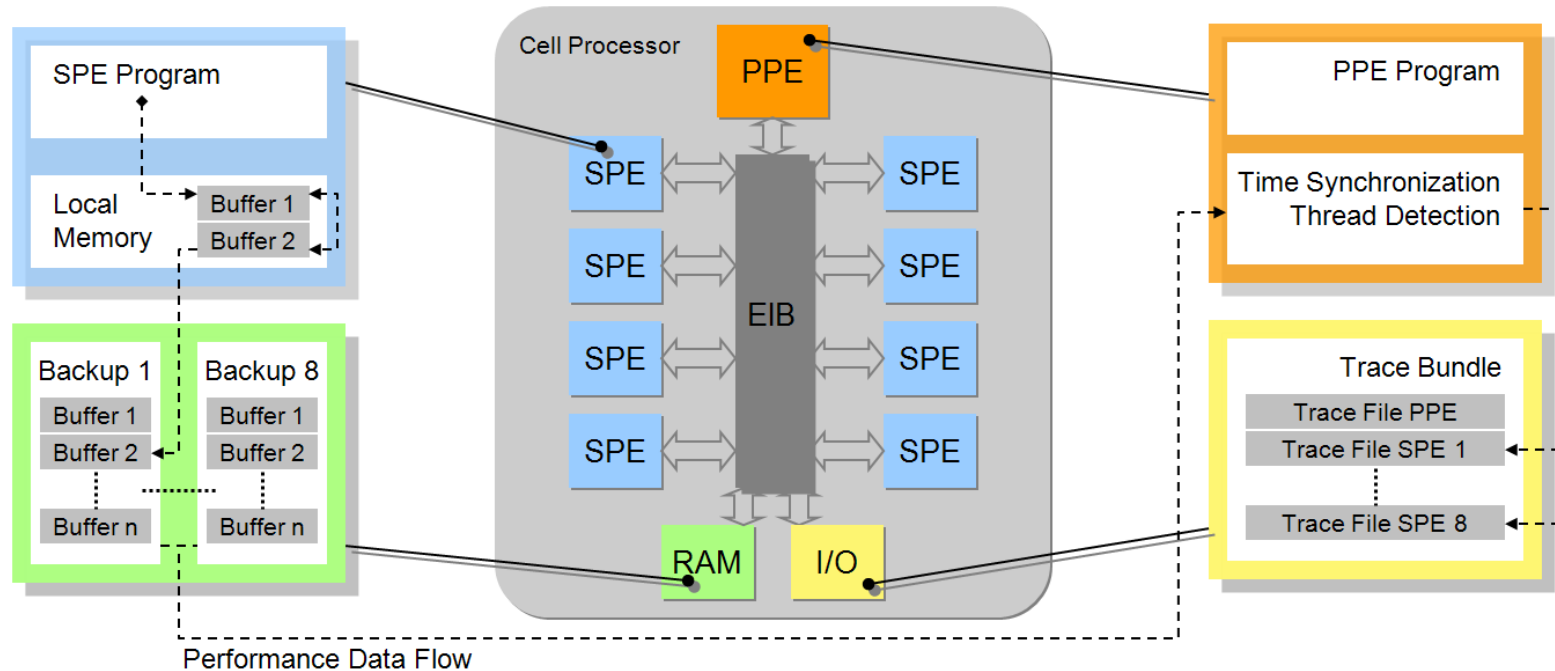
- GUI for profiling, based on Qt
 - Simplifies usage:
 - No extra config files
 - Multiple runs automatically
 - Charts for visual analysis
 - Features
 - GPU Time Summary Plot: find long running kernels
 - GPU Width Plot: simplified Timeline (GPU, memcpy only)
 - Comparison plots (summary for two sessions)
 - Advantages
 - Easy to use, works on all cuda-platforms (Windows, Linux, Mac)
 - Disadvantages
 - No zooming
 - Multiple runs
 - No support for CPU-Tracing

CUDA Visual Profiler (Eigenvalues; Width Plot)



- Most important summaries
- BUT: No zooming!
- What do the host CPUs do in the meantime?

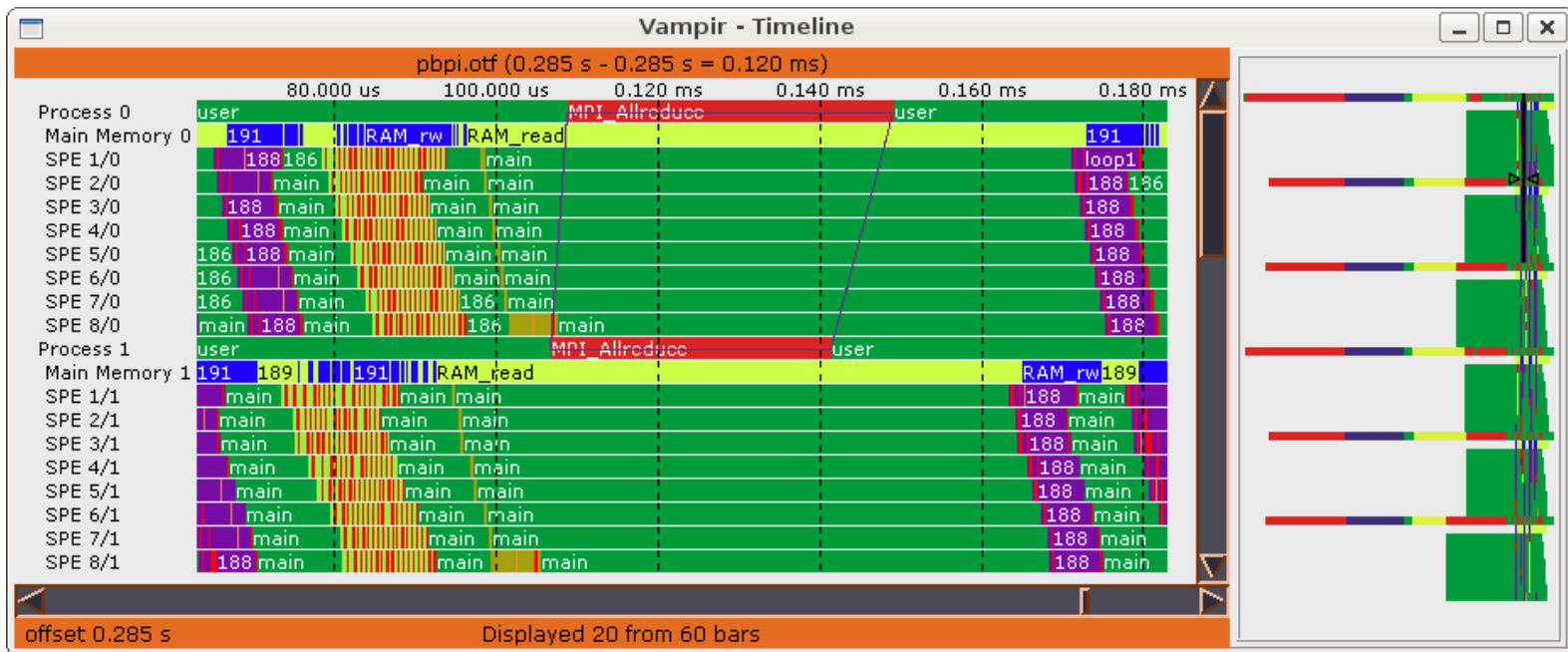
Special Solution: VampirTrace for CellBE



- Concept for Performance Tracing on Cell/B.E.
 - CellTrace, prototype integration in VampirTrace
 - Typical overhead: less than 5 percent
 - Fine grained event recording (resolution within 100s of nanoseconds)

CellBE Traces visualize in „Standard“ Vampir/VampirServer

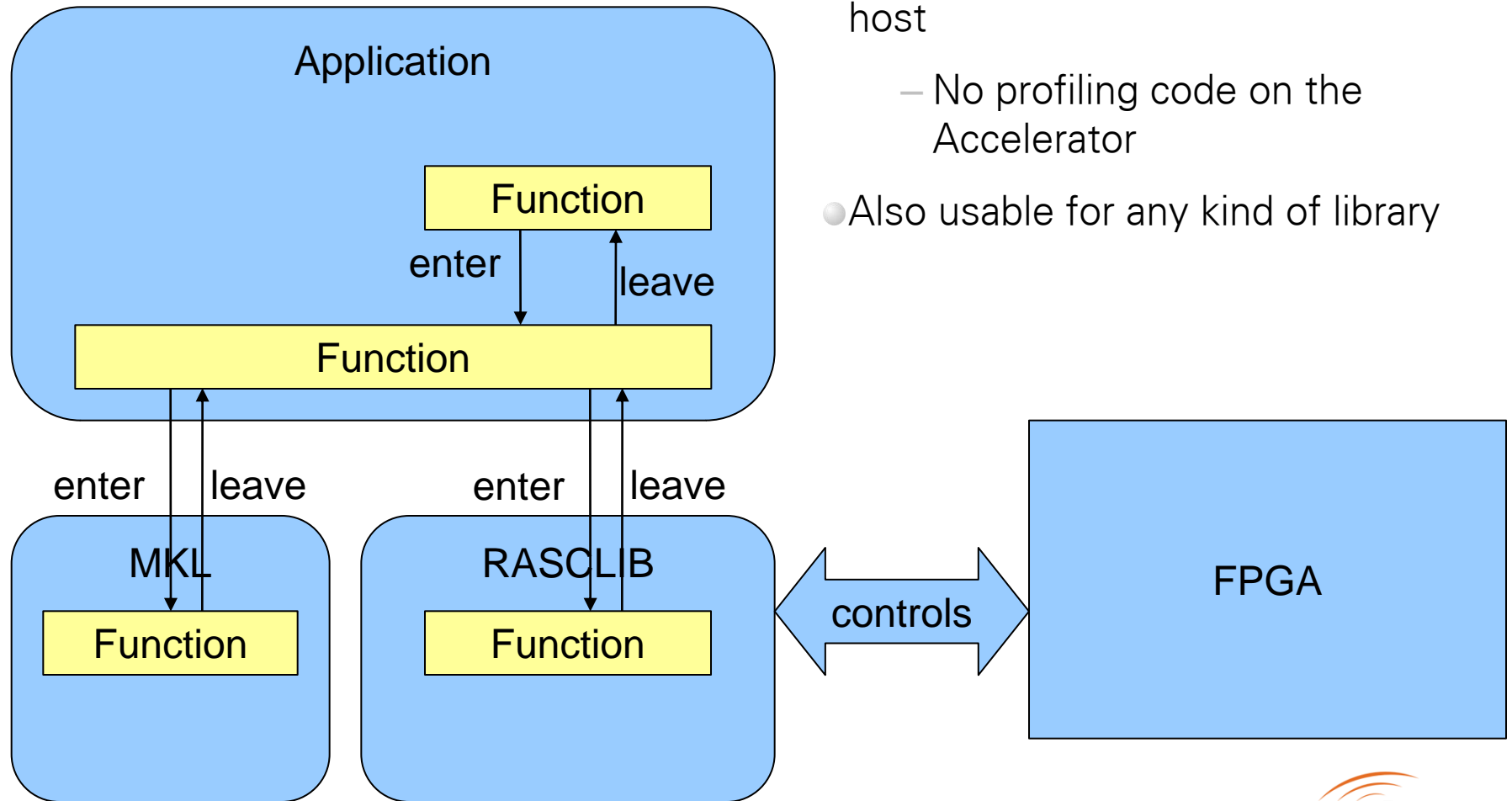
- Visualization of Traces with Vampir
 - Creates valuable insight into the runtime behavior of Cell applications
 - Intuitive performance visualization and verification
- Support for large applications with hybrid Cell/B.E. and MPI parallelism



VampirTrace API Tracing

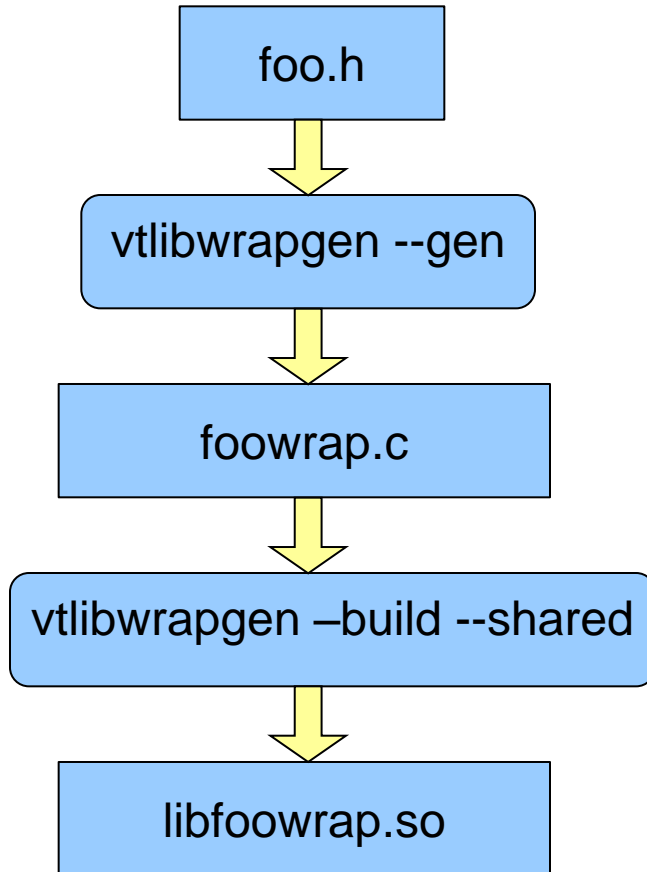
- Available since VampirTrace 5.8

Motivation



- Visualize Co-Processor usage by looking at library calls from the host
 - No profiling code on the Accelerator
- Also usable for any kind of library

Workflow



- Header-File of a(ny) library as source
- Generated wrapper functions use VampirTrace API
- Wrapper functions can be adapted (to include more information)
- Also works for static builds

LD_PRELOAD=\$PWD/libfoowrap.so <executable>

Filter

- Some libraries are quite large (MKL 10: 7979 function declarations)
- Apply VampirTrace filters also to wrapper generation
- Usable for function names and file names in/of the header file
- Top down priorities

```
/usr/* -- 0  
cblas_* -- -1  
clapack_* -- -1
```

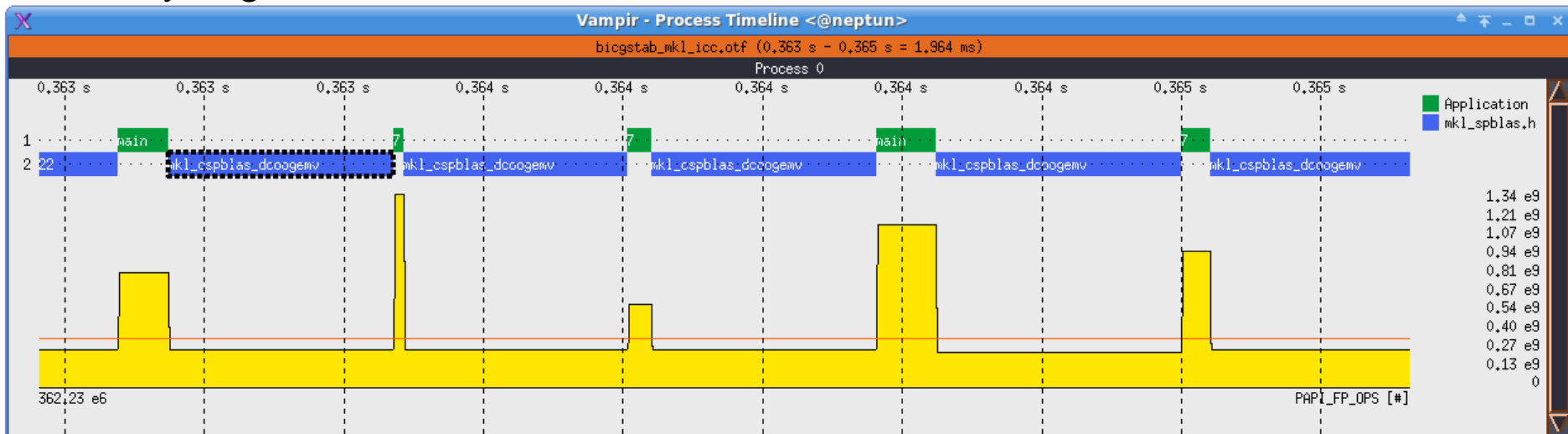
Example: Bicgstab

- Iterative equation solver
- MKL for matrix-vector-operations on sparse matrices
- Uses only one MKL header file: mkl_spblas.h

What you need to do:

- `vtlibwrapgen --gen -o mklwrap.c -f filter.default $MKL_INC/mkl_spblas.h`
- `vtlibwrapgen -build -shared -o libmklwrap mklwrap.c`
- `LD_PRELOAD=$PWD/libmklwrap.so ./bicgstab`

What you get:



VampirTrace CUDA Support

- Special Beta of VampirTrace 5.8
- Supports CUDA Versions 2.1-2.3

Beta Release (our Christmas present 😊)

Currently only CUDA Runtime API-Tracing

- Supports CUDA 2.1-2.3
- Runtime API hidden behind CUDA compiler (subject to change)

Use known metrics for parallelization

- Map GPUs to Threads
- Memory transfers = Thread communication

Statistics reusable

- Message statistics, summary charts
- But confusing when adding MPI and CPU threads (overlapping metrics)

Counter support

- Difficult, currently only possible by post-mortem OTF merging

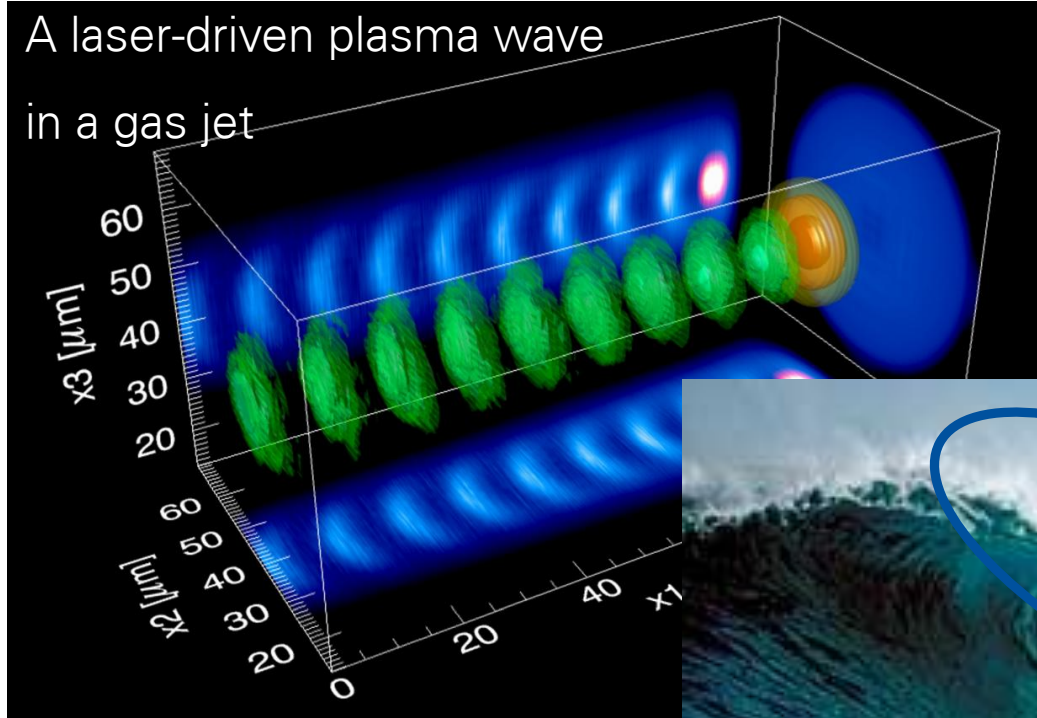
Support multiple GPU Streams

Visualize more GPU activity

An example: PiConGPU

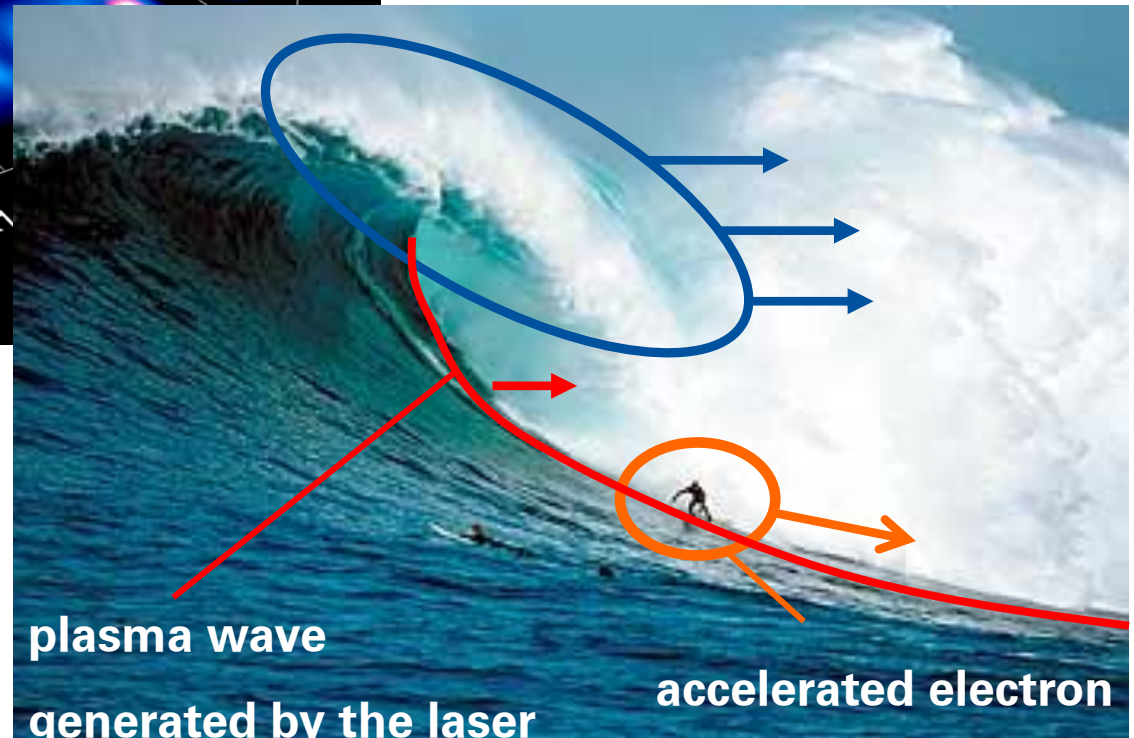
An Example: The Physics for Electron Acceleration

A laser-driven plasma wave
in a gas jet



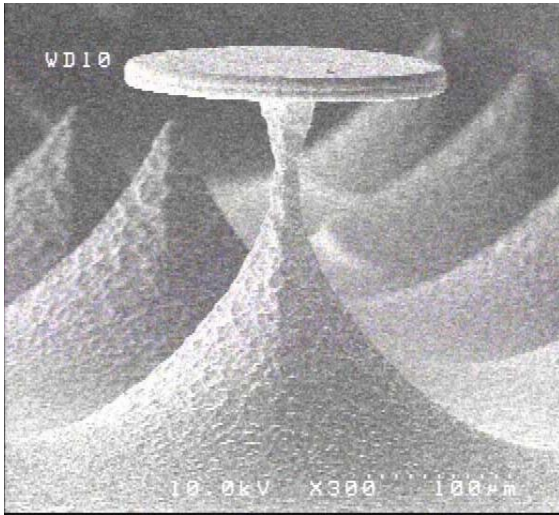
The Laser Pulse drives
wave-like Modulation
of the Electron Density

Electrons surf
on this Plasma Wave
which trails the Laser Pulse
At the Speed of Light

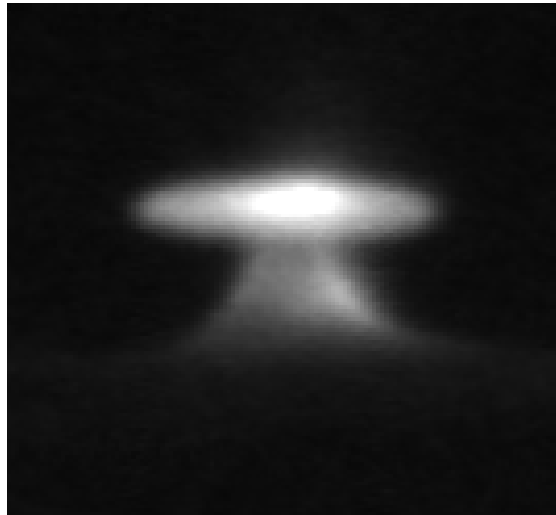


Simulation vs. Experiment (Pizza-Cone-Targets)

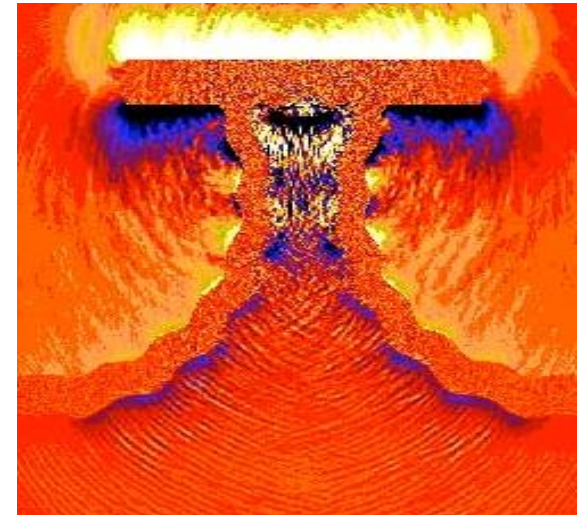
We know what we are doing...



Microscopic Image



X-ray Emission
during Experiment



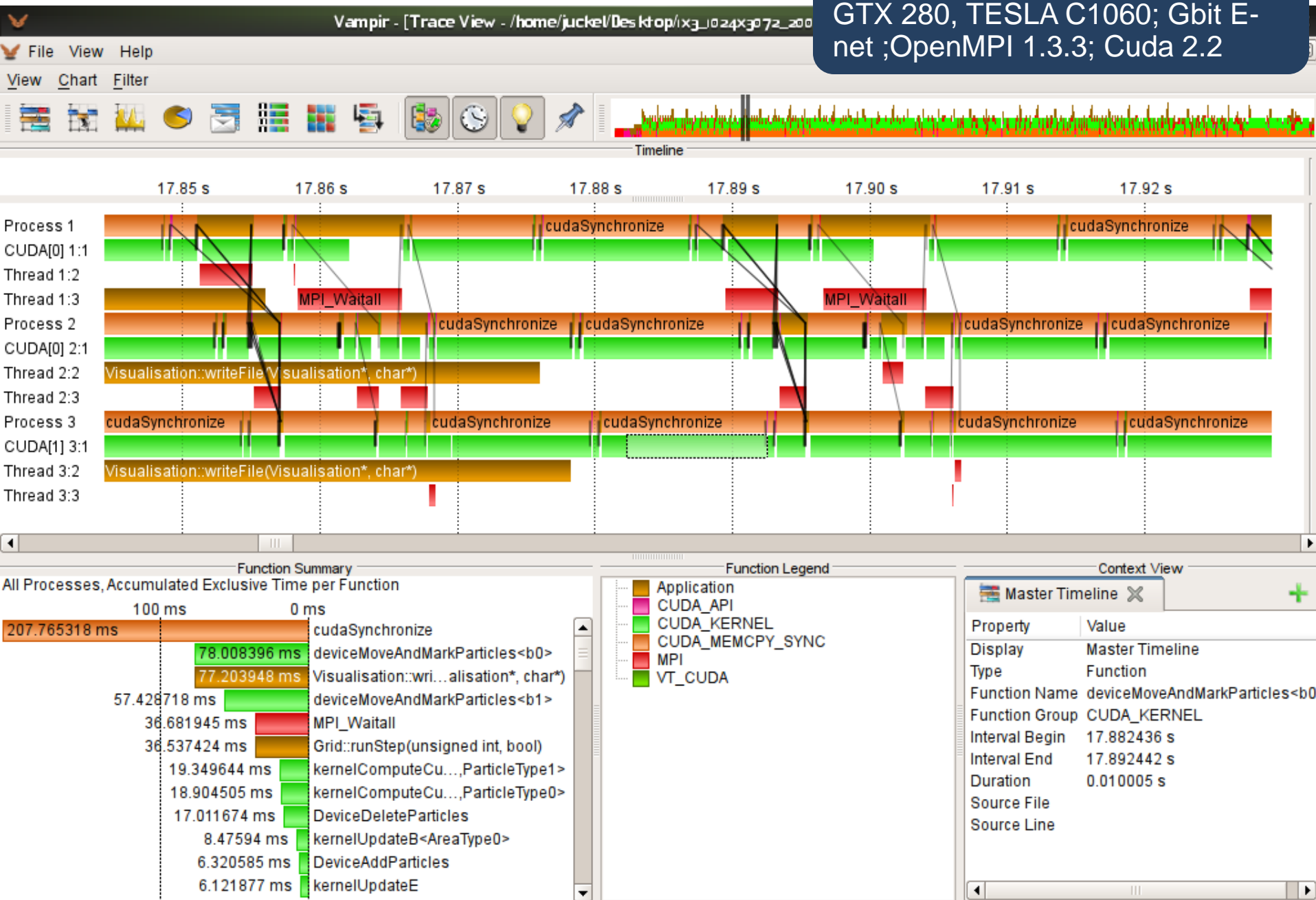
Simulation
of Field Distribution

...but it is hard to experimentally probe the
temporal evolution of the laser-target interaction
on a time scale of femtoseconds

O. Jäkel, DKFZ Heidelberg

What does it look like in Vampir?

Core i7 920 2.66 Ghz, 8GB RAM;
GTX 280, TESLA C1060; Gbit E-
net ;OpenMPI 1.3.3; Cuda 2.2



Summary/ Outlook

What has been accomplished?

Currently Solutions for three platforms in varying detail

- Cell -> extremely good (Standard Vampir, Special VampirTrace)
- GPU / FPGA -> only API tracing

Very low overhead

- Between 1 % (GPU/FPGA) and 5 % (Cell)

No need to learn new tools

- Interesting metrics are still the same (just a little more complex)

A couple of success stories with the new possibilities

- Understanding why FPGABLAST was so bad on our system
- A PiC implementation that the whole plasma physics community is extremely excited about
- A great tool to understand Cell applications

Support for OpenCL

Scalability of the tool in general

- Expand to more processes for tracing and visualization

Requests from other groups

- Help on parallelizing their CUDA codes
- Performance studies on their hybrid codes

Acknowledgements

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- Cell Tracing

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- PiConGPU (Linux port and Control infrastructure)

Thomas Ilsche (ZIH)

- API-Tracing
- RASCLIB VampirTrace support

Wolfgang Hönig (ZIH)

- PiConGPU (MPI parallelisation)
- VampirTrace integration of CUDA

Heiko Burau (FZD)

- PiConGPU work (Physics and CUDA kernels)